

## SEQUENCE LISTING

### 5 (1) GENERAL INFORMATION

(i) APPLICANT: Burnham, Martin K.

10 (ii) TITLE OF THE INVENTION: NOVEL XANTHINE PHOSPHORIBOSYL  
TRANSFERASE

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Dechert Price & Rhoads

(B) STREET: 997 Lenox Drive, Building 3, Suite 210

(C) CITY: Lawrenceville

(D) STATE: NJ

(E) COUNTRY: USA

20 (F) ZIP: 08543

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

25 (C) OPERATING SYSTEM: DOS

(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

30 (B) FILING DATE:

(C) CLASSIFICATION:

**(vii) PRIOR APPLICATION DATA:**

**(A) APPLICATION NUMBER:**

**(B) FILING DATE:**

5

**(viii) ATTORNEY/AGENT INFORMATION:**

**(A) NAME: Bloom, Allen**

10

**(B) REGISTRATION NUMBER: 29,135**

**(C) REFERENCE/DOCKET NUMBER:**

**(ix) TELECOMMUNICATION INFORMATION:**

**(A) TELEPHONE: 609-520-3214**

15

**(B) TELEFAX: 609-520-3259**

**(C) TELEX:**

**(2) INFORMATION FOR SEQ ID NO:1:**

20

**(i) SEQUENCE CHARACTERISTICS:**

**(A) LENGTH: 582 base pairs**

**(B) TYPE: nucleic acid**

**(C) STRANDEDNESS: double**

25

**(D) TOPOLOGY: linear**

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:**

30

ATGAAATTAT TAGAAGAGCG CATCCTCAAG GATGGGCATA TCTTGGGTGA  
TAACATCCTC 60

AAGGTAGATT CCTTTTAAAC CCACCAAGTT GACTTTAGCT TGATGCGAGA  
 GATTGGTAAG 120  
 GTTTTTGCGG AAAAATTTGC TGCTACTGGC ATTACCAAGG TCGTAACCAT  
 TGAAGCGTCG 180  
 5 GGTATTGCCC CAGCCGTTTT TACAGCTGAA GCCTTAAACG TTCCCATGAT  
 TTTCGCCAAA 240  
 AAAGCTAAGA ACATCACCAT GAACGAAGGC ATCTTAACTG CTCAAGTCTA  
 CTCCTTTACC 300  
 AAGCAGGTGA CCAGCACTGT TTCTATCGCT GGAAAATTCC TCTCACCAGA  
 10 GGACAAGGTT 360  
 TTGATTATCG ACGATTTCCT TGCTAATGGC CAAGCTGCTA AAGGCTTGAT  
 TCAAATCATC 420  
 GAACAGGCCG GTGCCACAGT CCAAGCTATC GGTATCGTGA TTGAGAAATC  
 CTTCCAAGAT 480  
 15 GGTCGTGATT TGCTTGAAAA AGCAGGCTAC CCTGTCCTAT CACTTGCTCG  
 CTTGGATCGT 540  
 TTTGAAAATG GTCAGGTCGT ATTTAAGGAG GCAGATCTCT AA  
 582

20 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- 25 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Leu Leu Glu Glu Arg Ile Leu Lys Asp Gly His Ile Leu Gly

1            5            10            15  
 Asp Asn Ile Leu Lys Val Asp Ser Phe Leu Thr His Gln Val Asp Phe  
           20            25            30  
 Ser Leu Met Arg Glu Ile Gly Lys Val Phe Ala Glu Lys Phe Ala Ala  
 5            35            40            45  
 Thr Gly Ile Thr Lys Val Val Thr Ile Glu Ala Ser Gly Ile Ala Pro  
           50            55            60  
 Ala Val Phe Thr Ala Glu Ala Leu Asn Val Pro Met Ile Phe Ala Lys  
 65            70            75            80  
 10 Lys Ala Lys Asn Ile Thr Met Asn Glu Gly Ile Leu Thr Ala Gln Val  
           85            90            95  
 Tyr Ser Phe Thr Lys Gln Val Thr Ser Thr Val Ser Ile Ala Gly Lys  
           100            105            110  
 Phe Leu Ser Pro Glu Asp Lys Val Leu Ile Ile Asp Asp Phe Leu Ala  
 15            115            120            125  
 Asn Gly Gln Ala Ala Lys Gly Leu Ile Gln Ile Ile Glu Gln Ala Gly  
           130            135            140  
 Ala Thr Val Gln Ala Ile Gly Ile Val Ile Glu Lys Ser Phe Gln Asp  
 145            150            155            160  
 20 Gly Arg Asp Leu Leu Glu Lys Ala Gly Tyr Pro Val Leu Ser Leu Ala  
           165            170            175  
 Arg Leu Asp Arg Phe Glu Asn Gly Gln Val Val Phe Lys Glu Ala Asp  
           180            185            190  
 Leu  
 25

**(2) INFORMATION FOR SEQ ID NO:3:**

**(i) SEQUENCE CHARACTERISTICS:**

- 30        **(A) LENGTH: 579 base pairs**  
           **(B) TYPE: nucleic acid**

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGAAATTAT TAGAAGAGCG CATCCTCAAG GATGGGCATA TCTTGGGTGA  
TAACATCCTC 60  
AAGGTAGATT CCTTTTAAAC CCACCAAGTT GACTTTAGCT TGATGCGAGA  
10 GATTGGTAAG 120  
GTTTTTGCGG AAAAATTTGC TGCTACTGGC ATTACCAAGG TCGTAACCAT  
TGAAGCGTCG 180  
GGTATTGCCC CAGCCGTTTT TACAGCTGAA GCCTTAAACG TTCCCATGAT  
TTTCGCCAAA 240  
15 AAAGCTAAGA ACATCACCAT GAACGAAGGC ATCTTAACTG CTCAAGTCTA  
CTCCTTTACC 300  
AAGCAGGTGA CCAGCACTGT TTCTATCGCT GGAAAATTCC TCTCACCAGA  
GGACAAGGTT 360  
TTGATTATCG ACGATTTTCCT TGCTAATGGC CAAGCTGCTA AAGGCTTGAT  
20 TCAAATCATC 420  
GAACAGGCCG GTGCCACAGT CCAAGCTATC GGTATCGTGA TTGAGAAATC  
CTTCCAAGAT 480  
GGTCGTGATT TGCTTGAAAA AGCAGGCTAC CCTGTCCTAT CACTTGCTCG  
CTTGGATCGT 540  
25 TTTGAAAATG GTCAGGTCGT ATTTAAGGAG GCAGATCTC 579

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys Leu Leu Glu Glu Arg Ile Leu Lys Asp Gly His Ile Leu Gly  
1 5 10 15  
Asp Asn Ile Leu Lys Val Asp Ser Phe Leu Thr His Gln Val Asp Phe  
10 20 25 30  
Ser Leu Met Arg Glu Ile Gly Lys Val Phe Ala Glu Lys Phe Ala Ala  
35 40 45  
Thr Gly Ile Thr Lys Val Val Thr Ile Glu Ala Ser Gly Ile Ala Pro  
50 55 60  
15 Ala Val Phe Thr Ala Glu Ala Leu Asn Val Pro Met Ile Phe Ala Lys  
65 70 75 80  
Lys Ala Lys Asn Ile Thr Met Asn Glu Gly Ile Leu Thr Ala Gln Val  
85 90 95  
Tyr Ser Phe Thr Lys Gln Val Thr Ser Thr Val Ser Ile Ala Gly Lys  
20 100 105 110  
Phe Leu Ser Pro Glu Asp Lys Val Leu Ile Ile Asp Asp Phe Leu Ala  
115 120 125  
Asn Gly Gln Ala Ala Lys Gly Leu Ile Gln Ile Ile Glu Gln Ala Gly  
130 135 140  
25 Ala Thr Val Gln Ala Ile Gly Ile Val Ile Glu Lys Ser Phe Gln Asp  
145 150 155 160  
Gly Arg Asp Leu Leu Glu Lys Ala Gly Tyr Pro Val Leu Ser Leu Ala  
165 170 175  
Arg Leu Asp Arg Phe Glu Asn Gly Gln Val Val Phe Lys Glu Ala Asp  
30 180 185 190  
Leu

**(2) INFORMATION FOR SEQ ID NO:5:**

**5 (i) SEQUENCE CHARACTERISTICS:**

**(A) LENGTH: 25 base pairs**

**(B) TYPE: nucleic acid**

**(C) STRANDEDNESS: single**

**(D) TOPOLOGY: linear**

**10**

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:**

**TCCTCAAGGT AGATTCCTTT TTAAC**

**25**

**15**

**(2) INFORMATION FOR SEQ ID NO:6:**

**(i) SEQUENCE CHARACTERISTICS:**

**(A) LENGTH: 20 base pairs**

**(B) TYPE: nucleic acid**

**(C) STRANDEDNESS: single**

**(D) TOPOLOGY: linear**

**20**

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:**

**25**

**CTCCTTAAAT ACGACCTGAC**

**20**